AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application:

LISTING OF CLAIMS:

1. (currently amended): An isolated protein comprising:

a) the 4-α-helix bundle motif formed from the α-helices of the ROP (repressor of primer) of SEQ ID NO:11 and

b) a redox centre,

wherein the redox centre comprises a ~~metal atom which is stable in different oxidation states~~haem group.

2. (canceled).

3. (previously presented): The protein of Claim 1, wherein the redox centre is bound to the protein, by coordination by one or more of histidine, leucine, methionine or cysteine residues.

4. (previously presented): The protein of Claim 1, wherein the redox centre is covalently bound to the 4-α-helix bundle motif formed from the α-helices of ROP.

5. (original): The protein of Claim 1 which has a redox mid-point potential in the range of -485 to +320mV.

6. (withdrawn): The protein of Claim 1 which has α-helix regions each having at least 60% similarity or identity with the α-helix regions of SEQ ID Nos: 1 and 3.

7. (withdrawn): The protein of claim 6, wherein said four α-helix regions are connected by loops.

8. (withdrawn): The protein of claim 7, wherein the four α-helices are joined in the order 1-1′-2′-2.

9. (withdrawn): The protein of Claim 1 which is formed by connecting two wild type ROP proteins to obtain the 4-helix bundle as one continuous polypeptide having at least 60% similarity or identity with SEQ ID No: 8.

10. (withdrawn): The protein of claim 9, wherein the histidine residues corresponding to H76, H78, H107 and H109 in sequence ID No. 8 are removed.

11. (withdrawn): The protein of claim 9, wherein histidine, leucine, methionine or cystein residues are introduced one or both positions corresponding to 56 and 113 in SEQ ID No: 8.

12. (previously presented): The protein of claim 1 which has a haem redox centre coordinated to the 4-α-helix bundle motif via two histidine residues.

13. (original): The protein of claim 12 which has a mid-point potential in the range -400mV to +300MV.

14. (canceled).

15. (previously presented): The protein of claim 1 which has a stability, measured as the unfolding free energy when denaturant is added to the protein of $\Delta G_{obs}H_2O$ is greater than or equal to y, wherein y is greater than or equal to 3.0 kcal/mol.

16. (withdrawn): A method of producing the protein of claim 1 comprising

i) expressing all four α-helices as a single polypeptide chain;

ii) engineering the required mutations to enable redox centre binding;

iii) expressing and purifying, or producing the redox centre binding mutant; and

iv) incubating the mutant with an excess of the redox centre to produce the protein.

17. (withdrawn): A nucleotide sequence which encodes the protein of claim 1 or a fragment thereof.

18. (withdrawn): A vector comprising the nucleotide sequence of claim 17.

19-20. (canceled).

21. (previously presented): An apparatus comprising the protein of claim 1 associated with the electrode.

22. (original): An apparatus according to claim 21 wherein the protein is absorbed onto an electrode.

23. (withdrawn - currently amended): A protein according to claim ~~2~~ 1 in which the redox centre is an iron sulfur centre.

24.-25. (canceled).

26. (withdrawn): A protein according to claim 6 in which the α-helix regions each have at least 80% similarity or identity with the α-helix regions of SEQ ID No: 1.

27. (withdrawn): A protein according to claim 9 in which the continuous polypeptide has at least 80% similarity or identity with SEQ ID No: 8.